



# FEATURES

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Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: eye; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 80.6%; Score 797.4; DB 12; Length 889;  
Best Local Similarity 99.5%; Pred. No. 5,9e-89;  
Matches 821; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

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QY 132 GGTCTGAGCCGCACTGGGCGCCGCTTGGCCACTGGCTCTTCTTCTGGGAGGCGGTCCTC 191
DB 61 GGTCTGAGCCGCACTGGGCGCCGCTTGGCCACTGGCTCTTCTTCTGGGAGGCGGTCCTC 120
QY 192 CCATGGCGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251
DB 121 CCATGGCGGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 252 TATCTTCTGAGCGCTCCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
DB 181 TATCTTCTGAGCGCTCCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 312 CTGGAGCAAGCCGAGGAGGAGATTTATGATGACTCTGGAGCAAGGCCCACTTTTGGCCAA 371
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QY 372 CTGGCGCGGCTCATCCAGGCGCAAGAGGCGCTGAGACTTGGGCACTTTCAGGCGTACTCC 431
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QY 432 GCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCGAGAGCGGCTGAGACTTGGGCGAGGAG 491
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DB 481 GAGCTCCGCTGAAGCGCGCTTGGAGAGCGCTTGGAGAGAGCTTGGCGCGCGGCGAGGCGC 540
QY 612 GGCACCTTGCAGCTGGCGCGCTGGTGGATGGAGCAAGAGAACTGCTCCGCTTACTACAG 671
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QY 672 CGCTGCTGAGCTGTGGAGCGCGGAGGAGATCTGCGCTCTCTCAAGTCTCTGTGGCGC 731
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QY 732 GGGAAAGTGTGAACTCTGAAAAGGGAGAGTGGCGCGAGAGTGTGTGGAAAAGCTTAAC 791
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QY 792 GAAAGCATCGGAGGAGAGCTCAAGGCTTCAATCAGGCTCTGCGCTTGGGCGAGATGACTC 851
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QY 852 ACCTT-GGCTTCAAGATCTAGGGCT-GAGCCCTTAGTAGAGGG 893

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DB 781 ACCTTGGGCTTCAAGATCTAGGGGTTGGGCCCTTAGTAGAGTGG 825

RESULT 2  
CB852030/LOCUS  
DEFINITION  
CB852030  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 771)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: McCray, PB  
McCrack Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 FORWARD  
POLYA=yes.

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

## FEATURES

source

Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/issue\_type="Human Lung Epithelial cells"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-FNO"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a  
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UI-CF-FNO is a subtracted cDNA library derived from two  
normalised Human lung epithelial cell libraries (EN1 and  
DUI) The library was subtracted according to according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. For additional information, contact:  
bento-soares@uiowa.edu  
TAG\_SEQ=None found"

## ORIGIN

Query Match 77.1%; Score 762.6; DB 14; Length 771;  
Best Local Similarity 99.5%; Pred. No. 1.2e-84;  
Matches 765; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 771 GCTTCCCCCGAGAGACCGCGCTGTGACAGATCTTGAAGCCGCTCATCGGAGAGCA 712
QY 281 CCGGCGCTGCGAGAGCTGAGCTGAGCTGAGAGAGCGCGAGGGGATTTATGAT 340
DB 711 CCGGCGCTGCGAGAGCTGAGCTGAGCTGAGAGAGCGCGAGGGGATTTATGAT 652
QY 341 GAGCTGAGAGAGCGCGAGCTTGGAGCAAGCTTGGCGGAGGCTCATCCAGGCAAGAGGC 400
DB 651 GAGCTGAGAGAGCGCGAGCTTGGAGCAAGCTTGGCGGAGGCTCATCCAGGCAAGAGGC 592

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RESULT 4	CA77547	756 bp	mRNA	linear	EST 03-DEC-2002
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	similar to TR:085769 085769 HYPOTHETICAL 24.8 KD PROTEIN. ;, mRNA				
sequence.					
ACCESSION	CA77547				
VERSION	CA77547.1	GI:26015422			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 756)				
	Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemshaha, I., Searce, M., Bressell, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wille, T., Martin, J., Blisatn, A., Schmitt, A., Theising, B., Rilter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.				
TITLE	Endocrine Pancreas Consortium				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40bp from Gibco High quality sequence stop: 462. Location/Qualifiers 1..756 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6217933" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_id="HR85 islet" /note="Organ: Pancreas; Vector: pluescript SK(-); Site_1: Not; Site_2: XhoI; cDNA made by oligo-dt priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."				
FEATURES					
SOURCE					
Query Match	74.4%	Score 736	DB 14	Length 756	
Best Local Similarity	99.2%	Pred. No. 2.2e-81			
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Db	282	CCGCGCGTGGAGAGCCGCGCTGTGGAGATCTTGAGCGCGCTCATGCGGAGAC	341		
Y	696	CCGCGCGTGGAGAGCCGCGCTGTGGAGATCTTGAGCGCGCTCATGCGGAGAC	637		
Db	342	ACCTGCGAGAGCGCGCGCTGTGGAGATCTTGAGCGCGCTCATGCGGAGAC	401		
Y	636	ACCTGCGAGAGCGCGCGCTGTGGAGATCTTGAGCGCGCTCATGCGGAGAC	577		

FEATURES	SOURCE
LOCUS	BF663323
DEFINITION	602144463p1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297911 5', mRNA sequence.
ACCESSION	BF663323
VERSION	BF663323.1 GI:119372218
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 1006)
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapds-remail.nih.gov">cgapds-remail.nih.gov</a> Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: L10M152 row: m column: 16 High quality sequence stop: 745. Location/Qualifiers
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 /clone\_lib="NIH\_MGC\_48"  
 /note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(9). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.9%; Score 721; DB 10; Length 1006;  
 Best Local Similarity 90.9%; Pred. No. 1,4e-79;

Matches 835; Conservative 0; Mismatches 75; Indels 9; Gaps 6;

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QY 139 CCGCACTGGGGCGCGCTTCGCACTGGCTCTTCTTGGGGAGGCGGTGCCCTCCATGAC 198
DB 62 CCGCACTGGGGCGCGCTTCGCACTGGCTCTTCTTGGGGAGGCGGTGCCCTCCATGAC 121
QY 199 GAGGCGGCGAGAGCACTGCTTCCCCCGAGAGAGCGCGCTGAGGATCTTTC 258
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DB 242 AGCGGAGGGGATTTCTATGATGACCTTCCGAGACAGAGCCAGCTTGGCCAACTGGGCG 301
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DB 302 GGGTCATCAGAGCCAGAGGCGCTGAGCTGGGACCTTCAAGGGCTACTCCGCGCC 361
QY 439 CCTTGGCTTCCGCTGCGCGCGAGCGGCGCGCTGAGCTTCAAGGGCTACTCCGCGCC 498
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DB 482 GGGTGAAGCCCGCTTGGAGACCTTGAAGCAAGCTTGGAGCGAGCGAGCGAGCGAGCG 541
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QY 679 TGGAGCTGCGCGAGCGAGAGGATCTTCCGCGCTTCAAGAGTCC-TGTGCGCGGAGAG 737
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QY 855 -TTGGCTTCAAG-ATCTAGGGCTGGCCCTTACTAGTGGGCTCAAGGAGAGGTTG--C 909

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DB 782 TTGAGCCTTCAAGGATCTAGGGTGGCCCTTAAAGTGGGTGACAGCGACGGTTGGCC 841
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DB 842 TCGGGAACCCCTAGGATGGTCCCGGTTTAATCCGCACTAGCTGCTTGGGACACCC 901
QY 970 CAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 988
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 LOCUS  
 DEFINITION 602145812P1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309298 5',  
 mRNA sequence.  
 ACCESSION BF664198  
 VERSION BF664198.1 GI:11938093  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 (bases 1 to 921)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 UNPUBLISHED (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMIN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILMIN at:  
 http://image.llnl.gov  
 Plate: ILMIN182 row: h column: 03  
 High quality sequence stop: 726.

## FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4309298"  
 /tissue\_type="Primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_48"  
 /note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAAGAG(9). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.4%; Score 716; DB 10; Length 921;  
 Best Local Similarity 97.4%; Pred. No. 5,9e-79;  
 Matches 781; Conservative 0; Mismatches 15; Indels 6; Gaps 5;

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QY 79 GGGCCATGACCCAGCGGTGCCCCGAGCTTCCTCCGTCGCCGCGCCGCTGAGCCTTGGCTCAG 138
DB 2 GGGCCATGACCCAGCGGTGCCCCGAGCTTCCTCCGTCGCCGCGCGCTGAGCCTTGGCTCAG 61
QY 139 CCGCACTGGGGCGCGCTTCGCACTGGCTCTTCTTGGGGAGGCGGTGCCCTCCATGAC 198
DB 62 CCGCACTGGGGCGCGCTTCGCACTGGCTCTTCTTGGGGAGGCGGTGCCCTCCATGAC 121
QY 199 GAGGCGGCGAGAGCACTGCTTCCCCCGAGAGAGCGCGCTGAGGATCTTTC 258

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Dp	122	CAGGCGCGGGAGAGCAGTGCCTCTGTTCCCCCGGAGGACAGCGCGCTGTGGCAGTACTCTTC	181
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Dp	182	TGAGCGCGCTCCATGGGGGAGACCCGGCGCCTCGAAGCTTGAGGCTGTGACCCCTGGAGC	241
Qy	319	AGCCGACAGGGGANTCTATGATGACCTGGGAGCAGGCCAGGCTTTGGGCAACCTGGAGCG	378
Dp	242	AGCGGCAAGGGGATCTTATGATGACCTGGAGCAGGCCAGGCTTTGGGCAACCTGGAGCG	301
Qy	379	GGCTCATCCAGGCCAAGAGGCGCTTGGACCTTGAGCACTTTCAGGCTACTCTCGGCGTTGG	438
Dp	302	GGCTCATCCAGGCCAAGAGGCGCTTGGACCTTGAGCACTTTCAGGCTACTCTCGGCGTTGG	361
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Dp	421	CCCCGAGCTGGGACGAGCCCTGTGGAGGCAAGCCGAGCCGAGGACAAATATCGACTTCC	480
Qy	559	GGCTGAAACCCGCTTTGGAGATCCTTGGACGAGCTCTGGCGGCGGAGCGAGGCGACTTCC	618
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Qy	679	TGCAAGTGTCTGCAACCCCGAGGCACTCTGCGCGCTCTTCAAGATCTTGTGGCGGGGAAAG	738
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Qy	739	TGCTGCAACCTCCGAAAGGGGACGTTGGGCGGCGAGTGTGTGGAACTTAACGAAACGA	798
Dp	660	TGCTGCAACCTCCGAAAGGGGACGTTGGGCGGCGAGTGTGTGGAACTTAACGAAACGA	718
Qy	799	TCCGGCGGGAGCGTCAAGGCTTACATCAACCTCTGCCCCCTGGGCGATGAGACTGCTTGG	858
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QY	878	GCCCTAGTAGTGGGCTTCGAGGAGGAGTTGCTGCGGAACCCGAGGAATTGACCTGAGT	937
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QY	938	TTTAATTCGAAAAATTAAGTGGGGCTGGGACACAAAAAATTTTTTTTTTTTTTTTTTTT	989
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RESULT	8
CB852718	
LOCUS	
DEFINITION	CB852718 750 bp mRNA linear EST 22-Apr-2003
ACCESSION	U1-CF-FN0-afl-p-08-0-U1.s1 U1-CF-FN0 Homo sapiens CDNA clone U1-CF-FN0-afl-p-08-0-U1 3', mRNA sequence. CB852718

VERSION	CB852718.1	GI:30047716
KEYWORDS	EST.	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE

Euhairy, Ota.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 750)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and substructure: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477

PUBMED 8809548  
COMMENT Contact: McCray, PB

McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel.: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics ([www.resgen.com](http://www.resgen.com)) or from Open Biosystems  
([www.openbiosystems.com](http://www.openbiosystems.com)).  
Seq primer: M13 FORWARD  
POLYA=No.

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Location/Qualifiers
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_id="UI-CF-FNO"
/notes="Organ: lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site: 1: Score 1; Site 2: Not 1;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized human lung epithelial cell libraries (EN1 and
DU1) The library was subtracted according to according to
Bonaldo, Lemon and Soares; Genome Research, 6:791-806,
1996. For additional information, contact:
dento-soares@uiowa.edu
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Query Match	70.8%; Score 699.8; DB 14; Length 750;
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Db	1	GGGGGCGCGTCAACACACCTCTCTCCCGTCAAGGAGAGCGGTGCGCCCCCATAGCGAGGCGGAG	60
QY	208	GAGAGCAATGCTCTGCTTCCCTCCCGAGAGCAACCGCTTGTGGCAGTATCTTTCAGCGCT	267
Db	61	GAGACAGATGCTGCTTCCCTCCCGAGAGCAACCGCTTGTGGCAGTATCTTTCAGCGCT	120
QY	268	CCATGCGGGAGACCCCGGCGCTGCGAACCCTGAAGCTGTGACTCTGAGACAGCCGAGG	327
Db	121	CCATGCGGGAGACCCCGGCGCTGCGAACCCTGAAGCTGTGACTCTGAGACAGCCGAGG	180
QY	328	GGGATTCTATGATGACTCTGCGAGAGAGGCCAGCTCTTGGCGCAACTGTGCGCGGCTCATCC	387
Db	181	GGGATTCTATGATGACTCTGCGAGAGAGGCCAGCTCTTGGCGCAACTGTGCGCGGCTCATCC	240
QY	388	AGGCCAANAAGCGCTGGAAGCTTGCAGACCTTCAAGGCTACTCCGCCCTGAGCCCTGAGCC	447
Db	241	AGGCCAANAAGCGCGTGGAGCTTGGAGCACTTTCAGCGGCTACTCCGCCCTGAGCCCTGAGCC	300
QY	448	TGCGCGTCCCGCGGAGCGGCGCGTGTGACTCTGCGAGGTGGAGAGCGGAGCGCCCGAGAG	507
Db	301	TGCGCGTCCCGCGGAGCGGCGCGTGTGACTCTGCGAGGTGGAGAGCGGAGCGCCCGAGAG	360
QY	508	TGGAGCGGCCCCCTGTGAGAGGAGCGGCCGAGGCGAGGACCAAGATGACCTCCGAGCTGAAGC	567
Db	361	TGGAGCGGCCCCCTGTGAGAGGAGCGGCCGAGGCGAGGACCAAGATGACCTCCGAGCTGAAGC	420
QY	568	CGCGCTTGGAGACCTCTGAGAGGAGCTGTGTGCGGTGGGCGAGGCGCGACCTTTCAGCTGG	627
Db	421	CGCGCTTGGAGACCTCTGAGAGGAGCTGTGTGCGGTGGGCGAGGCGCGACCTTTCAGCTGG	480
QY	628	CCGTGTGTGATGCGGAGCAAGAGAACTGCTCCGCTCTACGAGCGCTGCTCGAGCTGC	687
Db	481	CCGTGTGTGATGCGGAGCAAGAGAACTGCTCCGCTCTACGAGCGCTGCTCGAGCTGC	540
QY	688	TGCGACCCCGAGAGGATCTCTGCGCGTCTTCAGAGTCTGTGTGCGCGCGGAGAGGTGTGCAAC	747
Db	541	TGCGACCCCGAGAGGATCTCTGCGCGTCTTCAGAGTCTGTGTGCGCGCGGAGAGGTGTGCAAC	600
QY	748	CTCCGAAAGAGGAGAGTGTGCGGAGGTGTGCGAAACTTAAACGAAACGATCCGAGGAG	807
Db	601	CTCCGAAAGAGGAGAGTGTGCGGAGGTGTGCGAAACTTAAACGAAACGATCCGAGGAG	660
QY	808	ACGTCAAGGATCTACATCAGCTCTCTGCGCTTCGAGCGATGGAATCACTTGTGACTTCAAGA	867
Db	661	ACGTCAAGGATCTACATCAGCTCTCTGCGCTTCGAGCGATGGAATCACTTGTGACTTCAAGA	719
QY	868	TCTAGGAGCTGAGCCCTAGTGAAGTGGAGCTGAG	899
Db	720	TCTAGGAGCTGAGCCCTAGTGAAGTGGAGCTGAG	750

**RESULT 9**  
**BE796570**  
**LOCUS**  
**BE796570**  
**DEFINITION**  
 60159224F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:394646 5',  
 mRNA sequence.  
**ACCESSION**  
 BE796570  
**VERSION**  
 BE796570.1 GI:10217768  
**KEYWORDS**  
 EST.  
**SOURCE**  
 Homo sapiens (human)  
**ORGANISM**  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE**  
 1 (bases 1 to 772)  
 NIH-MGC <http://mgc.ncl.nih.gov/>.





Db 62 CGGACACTGGGCGCGCCTTCCGACACTGGCCTTCTTCTGGGAGGCGGTGCCCCCATGAC 121  
 Qy 199 GAGGCGCGGAGAGAGAGTCCCTGCTTCCCTCCGAGAGACCGCCTGTGGAGTATCTTC 258  
 Db 122 GAGGCGCGGAGAGAGAGTCCCTGCTTCCCTCCGAGAGACCGCCTGTGGAGTATCTTC 181  
 Qy 259 TGAGCGCGGCTCCATGGGAGAGACCGCGGCTGTCCGAAAGCTTGAAGCTTGAAGCTTGAAGC 318  
 Db 182 TGAGCGCGGCTCCATGGGAGAGACCGCGGCTGTCCGAAAGCTTGAAGCTTGAAGCTTGAAGC 241  
 Qy 319 AGCGCGAGGAGGATTTCTATGATGACCTTGAAGCA-GGCGCAAGCTTGTGGCAAGCTTGAAGC 376  
 Db 242 AGCGCGAGGAGGATTTCTATGATGACCTTGAAGCAAGCTTGTGGCAAGCTTGAAGCTTGAAGC 301  
 Qy 377 GCGGCTATCCAGGCGCAAGAGGCGCTGAGACTTGGGCACTTTCAC-GGGCTACTCCGCGC 435  
 Db 302 GCGGCTATCCAGGCGCAAGAGGCGCTGAGACTTGGGCACTTTCACGCTTGGGCTACTCCGCGC 361  
 Qy 436 TGGGCGCTGGCGCTGGGCGCTGGGCGCGGCGCGGCGGCTGGGCGCTGGGCGGCGGCGGCGG 494  
 Db 362 TGGGCGCTGGCGCTGGGCGCTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 421  
 Qy 495 CAGCGCGCGAGCTGGGAGCGGCGCTGTGAGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 554  
 Db 422 CAGCGCGCGAGCTGGGAGCGGCGCTGTGAGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 481  
 Qy 555 CTCCGCTGAAAGCGCGCTTGGAGACCTTGAAGCAAGCTTGGCGGCGGCGGCGGCGGCGGCGGCGG 614  
 Db 482 CTCCGCTGAAAGCGCGCTTGGAGACCTTGAAGCAAGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 541  
 Qy 615 ACCCTGAGAGTGGCGCGGCTGGGCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 673  
 Db 542 ACCCTGAGAGTGGCGCGGCTGGGCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 601  
 Qy 674 CTGCTGCAAGCTGGCGAGCGGCGGAGGCA-TCCCTGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 732  
 Db 602 CTGCTGCAAGCTGGCGAGCGGCGGAGGCA-TCCCTGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 661  
 Qy 733 GGAAGGTGCTGCAAGCTTCCGAAAGGAGGAGC-GTGGCGGCGGAGTGTGTGCGAAAGCTTAAAC 791  
 Db 662 GGAAGGTGCTGCAAGCTTCCGAAAGGAGGAGC-GTGGCGGCGGAGTGTGTGCGAAAGCTTAAAC 721  
 Qy 792 GAAAGGATCCGGGCGGAG-CGTCAAGGTCTTCAATCAGCTTCTTGGCGGCGGAGTGTGTGCGAAAGCTTAAAC 847  
 Db 722 GAAAGGATCCGGGCGGAG-CGTCAAGGTCTTCAATCAGCTTCTTGGCGGCGGAGTGTGTGCGAAAGCTTAAAC 778

RESULT 11  
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 LOCUS B0931589  
 DEFINITION AGENCOURT\_8795361 NIH\_MGC\_101 Homo sapiens cDNA clone IMAGE:6427775  
 ACCESSION B0931589  
 VERSION B0931589.1 GI:22346620  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 934)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph. D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Plate: LLM2613 row: e column: 24

High quality sequence stop: 532.  
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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:6427775"  
 /issue\_type="epidermoid carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_101"  
 /note="Organ: Lung; Vector: pOTB7, site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

Query Match 67.4%; Score 666.4; DB 13; Length 934;  
 Best Local Similarity 95.8%; Pred. No. 7.3e-73;  
 Matches 751; Conservative 0; Mismatches 21; Indels 12; Gaps 6;  
 Qy 87 ACCAGCGGCTGCGCGGCTCTCCGTCGCGCGCGGCTGGCGGCTGAGCGGCACTG 146  
 Db 1 ACCAGCGGCTGCGCGGCTCTCCGTCGCGCGCGGCTGGCGGCTGAGCGGCACTG 60  
 Qy 147 GCGCGCGCTTCCGCACTGGGCTCTTCTGGGAGCGGCGTGCCTCCCATGAGCGCGG 206  
 Db 61 GCGCGCGCTTCCGCACTGGGCTCTTCTGGGAGCGGCGTGCCTCCCATGAGCGCGG 120  
 Qy 207 CGAGAGAGTGGCGTCTCCCGCGGAGAGACAGCGCGCTGTGGAGATCTTCTGAGCGCG 266  
 Db 121 CGAGAGAGTGGCGTCTCCCGCGGAGAGACAGCGCGCTGTGGAGATCTTCTGAGCGCG 180  
 Qy 267 TCCATCGGAGAGACCGCGCGCTGCGAAGCTGAGGCTGTGACCCCTGGAGCGCGAG 326  
 Db 181 TCCATCGGAGAGACCGCGCGCTGCGAAGCTGAGGCTGTGACCCCTGGAGCGCGAG 236  
 Qy 327 GGGGATTTATATATGACCTTGCAGAGCGGCACTTGTGGCAACTGTGGCGGCTCATC 386  
 Db 237 GGGGATTTATATATGACCTTGCAGAGCGGCACTTGTGGCAACTGTGGCGGCTCATC 296  
 Qy 387 CAGGCGCAAGAGCGGCTGAGACCTTGGGCACTTACCGGCTACTTCCGCTTGGCGC 446  
 Db 297 CAGGCGCAAGAGCGGCTGAGACCTTGGGCACTTACCGGCTACTTCCGCTTGGCGC 356  
 Qy 447 CTGGCGCTCCCGCGGAGCGGCGCTGTGACCTTGGAGGCTGAGACCGGAGCGCGGAG 506  
 Db 357 CTGGCGCTCCCGCGGAGCGGCGCTGTGACCTTGGAGGCTGAGACCGGAGCGCGGAG 416  
 Qy 507 CTGGAGCGGCGCTGTGGAGGCGGCGGAGCGGAGCAAGATGACCTTCCGCTGAAG 566  
 Db 417 CTGGAGCGGCGCTGTGGAGGCGGCGGAGCGGAGCAAGATGACCTTCCGCTGAAG 476  
 Qy 567 CCGGCTTGGAGACCTTGGAGCGGCTGTGGAGGCGGAGCGGAGCGGAGCGGAGCGGAG 626  
 Db 477 CCGGCTTGGAGACCTTGGAGCGGCTGTGGAGGCGGAGCGGAGCGGAGCGGAGCGGAG 536  
 Qy 627 GCGGTGTGATGCGGAGCAAGAGAACTGCTCCGCTTCAAGAGCGGCTGCTGAGCTG 686  
 Db 537 GCGGTGTGATGCGGAGCAAGAGAACTGCTCCGCTTCAAGAGCGGCTGCTGAGCTG 596  
 Qy 687 CTGGCAAGCGGAGGATCTTCCGCTTCAAGAGCTTGTGGCGGAGGAGGCTGCGAA 746  
 Db 597 CTGGCAAGCGGAGGATCTTCCGCTTCAAGAGCTTGTGGCGGAGGAGGCTGCGAA 656  
 Qy 747 CTTCCGAAAGGAGGAGT--GGCGCGGAGGTGTG--CGAACTTAAAGGAGGCG--ATCC 801  
 Db 657 CTTCCGAAAGGAGGAGTGTGCGGCGGAGTGTGTGCGAAAGCTTAAAGGAGGCGGAGTCCG 716  
 Qy 802 GCGGAGAGTCA--GGGTTCATACAGCTCTCG--CCCTGGCGAGTGAAGTCACTCACTTGG 858

Db 717 GGGGGAAGCTCAAGGCTTACATCAAGCTCCCGGCGGCGAAGGAGACTACCTTGG 776  
Qy 859 CCTT 862  
Db 777 CCTT 780

## RESULT 12

LOCUS B0072503 1065 bp mRNA linear EST 02-APR-2002  
DEFINITION AGENCOURT 6838941 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5761696  
5' mRNA sequence.

ACCESSION B0072503  
VERSION B0072503.1 GI:19901549  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabds-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LLM12810 row: 1 column: 17  
High quality sequence stop: 489.

## FEATURES

source

1.1065  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5761696"  
/lab\_host="MDH10B"  
/clone\_lib="NIH MGC 122"  
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lung, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH\_MGC Library."

## ORIGIN

Query Match 63.7% Score 630; DB 13; Length 1065;  
Best Local Similarity 96.7% Pred. No. 2,1e-68;  
Matches 675; Conservative 0; Mismatches 20; Indels 3; Gaps 3;

Qy 1 GCGGAGCCGAGTCCGAGACCTGTCCAGAGAGCTCCAGCTCAGGTACCTGTACACGCC 60  
Db 1 GCGGAGCCGAGTCCGAGACCTGTCCAGAGAGCTCCAGCTCAGGTACCTGTACACGCC 60  
Qy 61 TCCGCGCGCTCTGCGCGCGCATGACCCAGCGGTGCGCGCTCTCGTGCCCGCG 120  
Db 61 TCCGCGCGCTCTGCGCGCGCATGACCCAGCGGTGCGCGCTCTCGTGCCCGCG 120  
Qy 121 CGCTGCGCTGAGGCTCAGCGCACTGGCGCGCGCTTGGCACTGGCTCTTCTGGGGA 180  
Db 121 CGCTGCGCTGAGGCTCAGCGCACTGGCGCGCGCTTGGCACTGGCTCTTCTGGGGA 180  
Qy 181 GCGGAGCCGAGTCCGAGACCTGTCCAGAGAGCTCCAGCTCAGGTACCTGTACACGCC 240  
Db 181 GCGGAGCCGAGTCCGAGACCTGTCCAGAGAGCTCCAGCTCAGGTACCTGTACACGCC 240

Db 181 GCGGAGCCGAGTCCGAGACCTGTCCAGAGAGCTCCAGCTCAGGTACCTGTACACGCC 240  
Qy 241 GCGTGGCAGTATCTTCTAGACCGCTTCATAGCGGAGACACCCGCGCTGGAAAGCTTGA 300  
Db 241 GCGTGGCAGTATCTTCTAGACCGCTTCATAGCGGAGACACCCGCGCTGGAAAGCTTGA 300  
Qy 301 GAGTGTGACCTCTGAGACGCGGAGGAGATTCTATGATGACCTGGAGAGGCGCCAGC 360  
Db 301 GAGTGTGACCTCTGAGACGCGGAGGAGATTCTATGATGACCTGGAGAGGCGCCAGC 360  
Qy 361 TCTTGGCCAACTGGCGCGGCTCTATCCAGGCGCAAGAGCGCTGACCTGGGACCTTCA 420  
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Qy 421 CGGCTACTCCTGCGCGCTGCGCGCTGCGCGCTGCGCGCGCGAGAGGCGCTGTGACT 480  
Db 421 CGGCTACTCCTGCGCGCTGCGCGCTGCGCGCTGCGCGCGCGAGAGGCGCTGTGACT 480  
Qy 481 GCGAGTGAAGCGCGACCGCGCGGAGCTGGAGACCGCTGTGAGGCGAGGCGCGG 540  
Db 481 GCGAGTGAAGCGCGACCGCGCGGAGCTGGAGACCGCTGTGAGGCGAGGCGCGG 540  
Qy 541 AGCAAGATGACCTTCCGCTGAAGCGCGCTTGGAGA CCTGGAAGAGCTGTGCGG 599  
Db 541 AGCAAGATGACCTTCCGCTGAAGCGCGCTTGGAGA CCTGGAAGAGCTGTGCGG 599  
Qy 600 GCGGAGGAGCGCGGACCTTGGAGGCTGGCGGTGGAGTGGAGCAAGAGAGTGGCT 657  
Db 601 GAGGAGGAGCGCGGACCTTGGAGGCTGGCGGTGGAGTGGAGCAAGAGAGTGGCT 657  
Qy 658 CCGCTTACTGAGAGCGCTGCTGCAAGCTGTGCGAGCC 695  
Db 661 CCGCTTACTGAGAGCGCTGCTGCAAGCTGTGCGAGCC 698

## RESULT 13

BMT68764

LOCUS BMT68764 625 bp mRNA linear EST 04-MAR-2002  
DEFINITION K-EST0051789 S14K402 Homo sapiens cDNA clone S14K402-11-A01 5',  
mRNA sequence.

ACCESSION

BMT68764

VERSION

BMT68764.1

KEYWORDS

GI:19098379

SOURCE

EST.

ORGANISM

Homo sapiens (human)

REFERENCE

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, D.M., Park, H.S., Kim, S. and  
Kim, Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Beon-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongseung@mail.kribb.re.kr  
Plate: 11 row: A column: 01  
High quality sequence stop: 625.

FEATURES

source

1.625  
Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="S14K402-11-A01"  
/cell\_line="K402"  
/lab\_host="Top10F"  
/note="Organ: Stomach; Vector: pTZ19Bp1; Site\_1: EcoRI;  
Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then dephosphorylated with tobacco acid pyrophosphatase (TAP). The dephosphorylated intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Beig method. The competent cells E. coli Top10F<sup>+</sup> by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 63.2%; Score 625; DB 12; Length 625;  
Best Local Similarity 100.0%; Pred. No. 1e-67;

Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 65 GCGGCTCTCTCCGCGCGCATGACCCAGCCGCTCTCCGCGCGCGCT 124
Db 1 GCGGCTCTCTCCGCGCGCATGACCCAGCCGCTCTCCGCGCGCGCT 60
QY 125 GCGGCTCTCTCCGCGCGCATGACCCAGCCGCTCTCCGCGCGCGCT 184
Db 61 GCGGCTCTCTCCGCGCGCATGACCCAGCCGCTCTCCGCGCGCGCT 120
QY 185 GTGCCCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
Db 121 GTGCCCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 245 GTGAGAGATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 304
Db 181 GTGAGAGATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 305 GCTGACCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
Db 241 GCTGACCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 365 GAGCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
Db 301 GAGCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 425 CTACTCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
Db 361 CTACTCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 485 GGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
Db 421 GGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 545 CAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
Db 481 CAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 605 CGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664
Db 541 CGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 665 CTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
Db 601 CTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 625
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RESULT 14  
Bg339399  
DEFINITION  
Bg339399 912 bp mRNA linear EST 27-FEB-2001  
602437508F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4555609 5',  
ACCESSION  
Bg339399.1 GI:13145837  
VERSION  
Bg339399.1  
KEYWORDS  
EST.

## SOURCE

## ORGANISM

Homo sapiens (human)

Rukavota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/MLML at:

http://image.llnl.gov

Plate: L10M1256 row: 0 column: 02

High quality sequence stop: 719.

Location/Qualifiers

1. 912

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4555609"

/tissue\_type="leiomyosarcoma cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGAACAGAG(G). Size-selected >500bp for average insert size

1 kb. Library constructed by Ling Hong in the Laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH\_MGC

Library."

## ORIGIN

Query Match 62.8%; Score 621; DB 12; Length 912;  
Best Local Similarity 96.5%; Pred. No. 2.8e-67;

Matches 742; Conservative 0; Mismatches 15; Indels 12; Gaps 10;

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Db 2 CTGCGCGCGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 61
QY 133 GCTCAGCGGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192
Db 62 GCTCAGCGGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
QY 193 CATGCGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
Db 122 CATGCGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
QY 253 ATCTTCTGAGCGGCTTCATGCGGAGAGAGAGAGAGAGAGAGAGAG 312
Db 182 ATCTTCTGAGCGGCTTCATGCGGAGAGAGAGAGAGAGAGAGAGAG 241
QY 313 TGGAGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
Db 242 TGGAGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
QY 373 TGGCGGAGCTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
Db 302 TGGCGGAGCTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
QY 433 CCTGAGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCG 492
Db 362 CCTGAGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCG 420
QY 493 CGCAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
Db 362 CCTGAGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCGGCTTGGCG 420
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Db 421 CGAGGCCCGGAGCTGGGACGG-CCTGTGAGGAGCGGCGGAGCACAAGATCG 479

QY 553 ACCTCCGGCTGAGAGCCCGCTTGGAGACCTGGACGAGCTGCGGGGGGAGAGCCG 612

Db 480 ACTCCGGCTGAGAGCCCGCTTGGAGACCTGGAGAGCTGCGGGGGGAGAGCCG 539

QY 613 GCACCTTCGACGCTGGCCGCTGTGTGATGCGGACAGAGAACTGCTCCGCTACTACGAG 672

Db 540 GCACCTTCGACGCTGGCCGCTGTGTGATGCGGACAGAGAACTGCTCCGCTACTACGAG 596

QY 673 GCTGCTGACGCTGCTGCGACCCGAGGACATCTCTGCGCTCTGAGAGTCTGTGGCGG 732

Db 597 GCTGCTGACGCTGCTGCGACCCGAGGACATCTCTGCGCTCTGAGAGTCTGTGGCGG 654

QY 733 GGAAGGTGCTGCAACCTCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 792

Db 655 GGAAGGTGCTGCAACCTCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 710

QY 793 AACGATCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 841

Db 711 AACGATCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 758

RESULT 15  
AK054334  
LOCUS 2243 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone.F330016121 product:weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus], full insert sequence.

ACCESSION AK054334  
VERSION AK054334.1 GI:26344156  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE Carninci, P. and Hayashizaki, Y.  
JOURNAL High-efficiency full-length cDNA cloning  
MEDLINE 99279253  
PubMed 10349636

REFERENCE  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20493374  
PubMed 11042159

REFERENCE  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, Y., Nishi, K., Katsunuma, T., Tashiro, H., Itoh, M., Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsui, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PubMed 11076861

REFERENCE  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
MEDLINE 11076861  
PubMed 11076861  
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation

# JOURNAL REFERENCE AUTHORS

of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2243)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanakawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohse, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT  
Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

## FEATURES SOURCE

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## ORIGIN

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QY	303	CTGCTGACCCCTGGAGAGACCGGAGGGGAGATTCTATATGATGACTTGCAGACAGGCCACTC	362
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QY	363	TTGGCCAACTGGCGCGGCTCATCCAGAGCCAAAGAGCGCTGGAACCTGGGCACTTCAAG	422
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QY	483	GAGTGGAGATCGCGAGCCCCCGGAGCTGGGAGCGGCCCTGTGAGAGCAGGCCGAGGCGAG	542
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QY	603	GGCGAGGCGGCACTTCGACGTGGCGCGTGGTGAATGGGGAACAAGAGAACTGTCTCCGC	662
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QY	663	TACTACGAGCGCTGCTGCACTGTGCGACCCCGAGGAGCATCCTGACCGCTCTCGAAGTC	722
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QY	783	AACCTAAACGAACGATATCCGCGGGGAGCTCAGGGTCTACATCAGCTCTGCGCCCTGAGC	842
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QY	843	GATGAGCTACACTTGGCGCTCAAGATCMAAGGCTGGCCCCCTAAGTAAGTGGGCTCGAGGGA	902
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QY	903	GGGTTCCTTGGGAACCCGAGGAATTGACCTCGATTTAAATTTGGAATAAATAAG	956
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RESULT 16	
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LOCUS	AK007659
DEFINITION	AK007659 919 bp mRNA linear HTC 20-SEP-2003
	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
	enriched library, clone:1810030M08 product:weakly similar to
	PUPATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus],
	full insert sequence.
ACCESSION	AK007659
VERSION	AK007659.1 GI:12841341
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)

JOURNAL PUBMED	99279253
AUTHORS	10349636
TITLE	Itch, M., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.
JOURNAL MEDLINE PUBMED	20499374 11042155
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsumai, T., Teshito, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamanouchi, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, Y., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawaj, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL MEDLINE PUBMED	Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL PUBMED	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL PUBMED	Nature 420, 563-573 (2002) 6 (Bases 1 to 919)
REFERENCE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Ari, A., Aono, H., Arawaka, T., Bono, H., Carninci, P., Fukuda, S., Fukushima, Y., Funuro, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itom, M., Izawa, M., Kaekawa, T., Kato, C., Kawai, U., Kojima, Y., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nemura, K., Numazaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shubata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
JOURNAL PUBMED	Direct Submission
REFERENCE	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-501-9222, Fax: 81-45-503-9216)
COMMENT	Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details.
TITLE	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGGAATCGCAAGACCTCTTTTTCCTTTTTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rct = 20.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGGGGCCGAAATTACTTGAGTAATAATTAATCCCCCCCCC 3']. cDNA was cleaved with XhoI and SacI. Cloning sites, 5' end: XhoI, 3' end: SacI. Host: SOLr.
FEATURES	Location/Qualifiers
SOURCE	1..919





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 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 910)  
 Okazaki, I., Furuno, M., Kaekawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Mikawa, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I.,  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schombach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bull, C.,  
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 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 MEDLINE  
 PUBMED  
 12466851  
 COMMENT  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Saitama-cho, Tsukuba-shi, Ibaraki, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gs.c.riken.go.jp,  
 URL: http://genome-gsc.riken.go.jp/  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,  
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 Takeda, Y., Waki, K., Watabiki, A., Muramatsu, M., and Hayashizaki, Y.  
 Direct Submissions  
 Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN Integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site (http://genome-gsc.riken.go.jp) for  
 further details.

FEATURES  
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 Db 252 CTGTGAGACCCCTGAGAGCGGCGAGAGTCTATGATGACCTGAGAGCGGCGAGCTC 311  
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 Db 312 CTGGCCCACTTGGCGCGCTCATCCAGCGCAAGAGCGCGCTGAGCTTGGCACTTCA 371  
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 Db 432 GAGTGTGAGCGCGAGCGCGCGGAGCTGGAGCGCGCTTGGAGCGCGAGCGCGAG 491  
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RESULT 19  
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 LOCUS w37h07.x1 Soares NPL T GBC S1 Homo sapiens cDNA clone  
 DEFINITION IMAGE:2330365.3; Similar to TR:085769 085769 HYPOTHETICAL 24.8 KD  
 PROTEIN: , mRNA sequence.  
 A1692198  
 VERSION A1692198.1 GI:4969538  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 589)  
 NCICGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 761 Std Error: 0.00

FEATURES  
 source  
 High primer: -40UP from Gibco  
 location/Qualifiers  
 1..589  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2330365"  
 /lab\_host="DH10B"  
 /clone\_id="Soares\_NPL\_T\_GBC\_S1"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung KBHL19W, testis NBT, and B-cell  
 NCI-GAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo.

Query Match 59.2%; Score 585.8; DB 9; Length 589;  
 Best Local Similarity 99.7%; Pred. No. 6.7e-63;  
 Matches 587; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 387 CAGCCCAAGAGGCGCTGAGACCTTGGAGCGCGAGCTTGGAGCGCGAGCTTGG 446  
 Db 589 CAGCCCAAGAGGCGCTGAGACCTTGGAGCGCGAGCTTGGAGCGCGAGCTTGG 530  
 QY 447 CTGGCGCTGCGCGCGGAGCGCGCTGAGCTTGGAGCGCGAGCTTGGAGCG 506  
 Db 529 CTGGCGCTGCGCGCGGAGCGCGCTGAGCTTGGAGCGCGAGCTTGGAGCG 470  
 QY 507 CTGGAGCGCGCGCTGAGAGCGCGAGCGCGAGCGAGCGAGCGAGCGAGCG 566  
 Db 469 CTGGAGCGCGCGCTGAGAGCGCGAGCGCGAGCGAGCGAGCGAGCGAGCG 410  
 QY 627 GCGGTGTGATGCGGAGCAAGAGAGTCTGCGCTTGGAGCGCGAGCTTGGAG 686  
 Db 627 GCGGTGTGATGCGGAGCAAGAGAGTCTGCGCTTGGAGCGCGAGCTTGGAG 635  
 QY 687 CTGCGACCCGAGAGCAATCTGCGCGCTTGGAGCGCGAGCTTGGAGCGCGAG 746  
 Db 289 CTGCGACCCGAGAGCAATCTGCGCGCTTGGAGCGCGAGCTTGGAGCGCGAG 230  
 QY 747 CTGCGAGAGAGAGAGCTGCGCGCGAGAGTGTGCGAGAACTTAAACGAGCG 806  
 Db 229 CTGCGAGAGAGAGAGCTGCGCGCGAGAGTGTGCGAGAACTTAAACGAGCG 170  
 QY 807 GACGTGAGGCTTCAATCAAGCGCTTGGAGCGCGAGCTTGGAGCGCGAGCTT 866  
 Db 169 GACGTGAGGCTTCAATCAAGCGCTTGGAGCGCGAGCTTGGAGCGCGAGCTT 110  
 QY 867 ATCTAGGCTGCGCGCTTGGAGCTTGGAGCGCGAGCTTGGAGCGCGAGCTT 926  
 Db 109 ATCTAGGCTGCGCGCTTGGAGCTTGGAGCGCGAGCTTGGAGCGCGAGCTT 50  
 QY 927 TGACCTGAGCTTAAATTCGAGAAATTAAGTGGGCTTGGAGCGAGCAAAA 975  
 Db 49 TGACCTGAGCTTAAATTCGAGAAATTAAGTGGGCTTGGAGCGAGCAAAA 1

RESULT 20  
 BG339315 1122 bp mRNA linear EST 27-FEB-2001  
 LOCUS BG339315  
 DEFINITION 602437607F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:455585 5',











QY 474 GTGACCTGGAGGTGGACGCGACGCCGCCGAGCTGGACGCGCCCTGTGGAGCAGGCC 533  
 DB 361 GTGACCTGGAGGTGGACGCGACGCCGCCGAGCTGGAGCAGGCCCATGTGGAAGCAGCA 420  
 QY 534 GAGCGGACACCAAGATCGACCTCCGCTGGAAGCCCGCTTGGAGACCTCTGACGAGCTG 593  
 DB 421 GAAGTGGACACCAAGATCGACCTCCGCTGGAAGCCCGCTTGGAGACCTCTGAGCTG 480  
 QY 594 CTGGCGGCGGCGAGCGCGGACCTTGCAGCGTGGCGGTGGATGCGGACCAAGAGAAC 653  
 DB 481 CTAGCGGCGGCGAGCGCGGACCTTGCAGCATAGCGGTGGATGCGGACCAAGAGAAC 540  
 QY 654 TGCTCGGCTACTTAAAGAGCTGCTGCTGACGCTGCTGCGACCGGAGGCAATCCTGCGCTG 713  
 DB 541 TGTACCGCTCTACTAGAGAGGCTGTCTGCGAGCTCTACGCTCCGAGGCGGTGCTGCTGTA 600  
 QY 714 CTGAGAGTCTGTGCGCGCGGAGAGTGTGCAACCTCCGAAAGGAGAGTGGCGGCGAG 773  
 DB 601 CTGAGAGTCTGTGCGCGCGGAGAGTGTGCAACCTCCGAGGCGGAGAGAGAGTGTGTA 660  
 QY 774 TGTGTGGGAAACTTAAACGAAAGCATCCGCGGCGGAGCTGAGGAGTCTACATGAGCTCTG 833  
 DB 661 TGTGTGGGAAACTTAAACGAAAGCATCCGCGGCGGAGCTGAGGAGTCTACATGAGCTCTG 720  
 QY 834 CCCCTGGCGGAGTGG-ACCTACCTTGGCTTCAAGATCTAGGAGCTGAGCTGAGCTGAG 890  
 DB 721 CCCCTGGAGTGGAGTGGCTTCTTGTGGCTTAAAGTCTAGGAGTCTAGGAGCTTAAAG 780  
 QY 891 GAGGCTGAGGAGGAGGAGTGGCTGAGGAGCCGAGG---AATTGACCTGAGTTTAAATTCG 947  
 DB 781 GAGGCTGAGGAGTGGAGGAGTGGAGGAGCCGAGGAGCTGAGCTGAGCTTAAATTCG 840  
 QY 948 AAAATTAAGTGGGAGTGGGAGCAAAAAA 989  
 DB 841 ACAATTAAGTGGAGTGGGAGCAAAAAA 882

RESULT 26  
 LOCUS AM157252/c  
 DEFINITION au3e01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783832 3' similar to TR:085769 085769 HYPOHETICAL 24.8 KD PROTEIN. ; mRNA sequence.

ACCESSION AM157252  
 VERSION AM157252.1 GI:6228653  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 582)  
 AUTHORS Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisels, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
 TITLE Wash-U-MC human EST Project  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through INM; contact the INM Consortium (info@image.lnl.gov) for further information.  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 419.

## FEATURES

source  
 1. 582  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2783832"

/sex="male"  
 /tissue\_type="frontal lobe"  
 /dev\_stage="5 months post-conception"  
 /lab\_host="DH10B"  
 /clone\_lib="Schneider fetal brain 00004"  
 /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site\_1: Sct1; Site\_2: Xho1; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-GAGAGAGAGAGAGTCAAGATCCTTAATTAATTAATCCCCCCCC-3' and 3' adaptor sequence: 5'-GAGAGAGAGAGTCAAGATCCTTAATTAATTAATCCCCCCCC-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LMCIB-Area Science Park, Trieste, Italy)."  
 ORIGIN

Query Match 57.1%; Score 564.4; DB 10; Length 582;  
 Best local Similarity 98.1%; Pred. No. 2.9e-60;  
 Matches 571; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 372 CTGGCGGCGCTCATCCAGGCGCAAGAGCGCTGAGCTGGACCTTACCGGCTACTCC 431  
 DB 582 CTGGCGGCGCTCATCCAGGCGCAAGAGCGCTGAGCTGGACCTTACCGGCTACTCC 523  
 QY 432 GCCCTGACCTTGGCGGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 491  
 DB 522 GCCCTGACCTTGGCGGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 463  
 QY 492 GCGGAGCGCGCGGAGCTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 551  
 DB 462 GCGGAGCGCGCGGAGCTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 403  
 QY 552 GACCTCGGCTGAAAGCGCGGCTTGGAGAGCCCTGAGAGCTGCTGCGGCGGCGGCGGCGG 611  
 DB 402 GACCTCGGCTGAAAGCGCGGCTTGGAGAGCCCTGAGAGCTGCTGCGGCGGCGGCGGCGG 343  
 QY 612 GGCACCTTGAAGCTGGCGGCTGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 671  
 DB 342 GGCACCTTGAAGCTGGCGGCTGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 283  
 QY 672 CGCTGCTGAGCTGTGCGAGCCCGGAGGAGCTGCGGCTGCGAGAGCTGTGGCGGCGG 731  
 DB 282 CGCTGCTGAGCTGTGCGAGCCCGGAGGAGCTGCGGCTGCGAGAGCTGTGGCGGCGGCGG 223  
 QY 732 GGGAGAGTCTGCAAGCTCCGAAAGGAGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 791  
 DB 222 GGGAGAGTCTGCAAGCTCCGAAAGGAGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 163  
 QY 792 GAAGCATCGGCGGAGCTGAGGAGCTGATCAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGG 851  
 DB 162 GAAGCATCGGCGGAGCTGAGGAGCTGATCAGAGCTGCGGCGGCGGCGGCGGCGGCGGCGG 103  
 QY 852 ACCCTGAGCTTGAAGATCTAGGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 911  
 DB 102 ACCCTGAGCTTGAAGATCTAGGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 43  
 QY 912 GGGAGAGCGGAGAGATTTAGAGCTGAGTGTAAATTTGAAATA 953  
 DB 42 GGGAGAGCGGAGAGATTTAGAGCTGAGTGTAAATTTGAAATA 1

RESULT 27  
 LOCUS CB181160  
 DEFINITION AGENCOURT 11381817 NIH MGC\_164 Mus musculus cDNA clone IMAGE:30240746 5', mRNA sequence.  
 ACCESSION CB181160  
 VERSION CB181160.1 GI:28177885



Matches 679; Conservative 0; Mismatches 163; Indels 4; Gaps 2;

QY 63 CCGCGGCTCTGCGCCCGCCATGACCAAGCGGTGCCCCGCTCTGCGCCCGCG 122

Db 16 CCGCGGCTCTGCGCCCGCCATGACCAAGCGGTGCCCCGCTCTGCGCCCGCG 75

QY 123 CTGGCCCTGGGCTGAGCGCGACCTGGGCGCCCGCTTCCGCACTGGGCTCTTCTGGGAGG 182

Db 76 CTGGCCCTGGGCTGAGCGCGACCTGGGCGCCCGCTTCCGCACTGGGCTCTTCTGGGAGG 135

QY 183 CCGTGGCCCCCATGGCGGAGCGCGGAGAGAGTCTGCTTCCCGCCGAGAGACAGCGCCG 242

Db 136 CCGTGGCCCCCATGGCGGAGCGCGGAGAGAGTCTGCTTCCCGCCGAGAGACAGCGCCG 195

QY 243 CTGGGAGCGATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCGCTGCGAGCTGAGG 302

Db 196 CTGGGAGCGATCTTCTGAGCGCGCTCCATGAGAGAGACACCGCGCGCTGCGAGCTGAGG 255

QY 303 CTGGGAGCGATCTTCTGAGCGCGCTCCATGAGAGAGACACCGCGCGCTGCGAGCTGAGG 362

Db 256 CTGGGAGCGATCTTCTGAGCGCGCTCCATGAGAGAGACACCGCGCGCTGCGAGCTGAGG 315

QY 363 TTGGCCAACTGGCGCGGCTCATCCAGGCGCAAGAGCGCTGGACTGGGCACTTCAAG 422

Db 316 CTGGCCAACTGGCGCGGCTCATTTAAGGCGCAAGAGAGCTGGAATCTGGAATCTTCAAG 375

QY 423 GGGTACTCCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCGCGCGCTGAGTCTGAG 482

Db 376 GGGTACTCCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCGCGCGCTGAGTCTGAG 435

QY 483 GAGGTGAGCG 542

Db 436 GAGGTGAGCG 495

QY 543 CACAAAGTCAAGCTCCGCGCTGAGAGCGCGCGCTTGGAGACCTTGAAGCGAGCTGAGCGCGCG 602

Db 496 CACAAAGTCAAGCTCCGCGCTGAGAGCGCGCGCTTGGAGACCTTGAAGCGAGCTGAGCGCGCG 555

QY 603 GGGGAGCG 662

Db 556 GGGGAGCG 615

QY 663 TACTAGAGCGCGCTGCGCTGAGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 722

Db 616 TACTAGAGCGCGCTGCGCTGAGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 675

QY 723 CTGGGCGCGCGAGAGGCTGCGCAACCTCCGAGAGGCGAGCGCGCGCGCGCGCGCGCG 782

Db 676 CTGGGCGCGCGAGAGGCTGCGCAACCTCCGAGAGGCGAGCGCGCGCGCGCGCGCGCG 735

QY 783 AACCTTAAAGAGCGATCCGCGCGGAGCGTCAAGGCTC-TACATCAAGCTTCTGCGCGCGCG 840

Db 736 AACCTTAAAGAGCGATCCGCGCGGAGCGTCAAGGCTC-TACATCAAGCTTCTGCGCGCGCG 795

QY 841 GCGATGAGAC-TACCTTGGCGCTTCAAGATCTAGGCGCTGCGCGCGCGCGCGCGCGCG 898

Db 796 AATGAGGCGCTTCTCCCTGCGCTTTAAATCTAGGCTTAAACCTTAAAGCGCGCTG 855

QY 899 GGGAGG 904

Db 856 GGGGCG 861

RESULT 29  
AM003514/c 578 bp mRNA linear EST 08-MAR-2000  
LOCUS AM003514  
DEFINITION wq66910.x1 NCI CGAP GC6 Homo sapiens cDNA IMAGE:2476290 3  
similar to TR:085765 085769 HYPOTHEICAL 24.8 KD PROTEIN.; mRNA

ACCESSION AM003514  
VERSION AM003514.1 GI:5850419  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 578)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgap@remail.nih.gov](mailto:cgap@remail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonafide, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/JMML at:  
[www.bio.linn.gov/bdip/image/image.html](http://www.bio.linn.gov/bdip/image/image.html)  
Insert Length: 799 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 462.  
Location/Qualifiers  
1. 578  
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/lab\_host="DH10B"  
/clone\_1ib="NCI CGAP GC6"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
from the normalized library NCI-CGAP GC6 was prepared, and  
as circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneids  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonafide."

ORIGIN

Query Match 55.5%; Score 549.2; DB 9; Length 578;  
Best Local Similarity 97.9%; Pred. No. 2, 1e-58;  
Matches 567; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

QY 393 AAGAGGCGCTGAGACTGCGGACCTTCAAGGCTACTCCGCTTGGCGCTTGGCGCG 452

Db 578 AAGAGGCGCTGAGACTGCGGACCTTCAAGGCTACTCCGCTTGGCGCTTGGCGCG 522

QY 453 CTGGCGCGCGAGCGGCGCGTGGTGAACCTGAGAGTGGAGCGCGAGCGCGCGCGCGCG 512

Db 521 CTGGCGCGCGAGCGGCGCGTGGTGAACCTGAGAGTGGAGCGCGAGCGCGCGCGCGCG 462

QY 513 CGGCGCTTGGAGGCGAGCGCGAGCGAGCGCAAGAGTGAACCTTCCGCTGAGAGCGCGCG 572

Db 461 CGGCGCTTGGAGGCGAGCGCGAGCGAGCGCAAGAGTGAACCTTCCGCTGAGAGCGCGCG 402

QY 573 TTGAGAGCCTTGAAGAGAGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 632

Db 401 TTGAGAGCCTTGAAGAGAGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 342

QY 633 GTGAGTGGCGAGCAAGAGAGAGTCTCCGCTCAAGAGCGTCTGAGAGCGTCTGAGCG 692

Db 341 GTGAGTGGCGAGCAAGAGAGAGTCTCCGCTCAAGAGCGTCTGAGAGCGTCTGAGCG 282

QY 693 CCGGAGGCGATCTTCCGCTCTCAAGAGTCTTGGCGCGCGGAGAGGCTGCAACTCCG 752

Db 281 CCGGAGGCGATCTTCCGCTCTCAAGAGTCTTGGCGCGCGGAGAGGCTGCAACTCCG 222

QY 753 AAGAGGAGCGTGGCGCGCGAGTGTGGCAACTTAAAGAGAGTCTGCGCGCGAGCGT 812

Db 221 AAGAGGAGCGTGGCGCGCGAGTGTGGCAACTTAAAGAGAGTCTGCGCGCGAGCGT 162

QY 813 AGGCTCATACAGCTCTGCCCCCTGGCCGATGACCTTGGCTTCAAGATCTAG 872  
 DB 161 AGGGTCTACATCAGCTCTGCCCCCTGGCCGATGACCTTGGCTTCAAGATCTAG 102  
 QY 873 GGGTGGCCCTAGTAGTGGGCTCGAGGGAGGTTGGCTGGGAGACCCCGAATGACCC 932  
 DB 101 GGGTGGCCCTAGTAGTGGGCTCGAGGGAGGTTGGCTGGGAGACCCCGAATGACCC 42  
 QY 933 TGAGTTTAAATTCGAAATAAAGTGGGCTGGGACACA 971  
 DB 41 TGAGTTTAAATTCGAAATAAAGTGGGCTGGGACACA 3

RESULT 30  
 AAS84408/c 620 bp mRNA linear EST 26-SEP-1997  
 LOCUS nm1803.s1 NCI CGAP Co9 Homo sapiens CDNA IMAGE:1090253 3'  
 DEFINITION similar to TR:G117130 G117130 PUTATIVE O-METHYLTRANSFERASE. ;  
 mRNA sequence.

ACCESSION AAS84408  
 VERSION AAS84408.1 GI:2369017  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 620)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

COMMENT Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,  
 M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html  
 Insert Length: 2341 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 345.  
 Location/Qualifiers

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 /clone="IMAGE:1090253"  
 /tissue\_type="Colon tumor RER+"  
 /lab\_host="DH10B"  
 /clone\_id="NCI CGAP Co9"  
 /note="Organ: Colon; Vector: pRT3D-Pac (Pharmacia) with a  
 modified polylinker, 1st strand cDNA was prepared from  
 RER+ colon tumor, and was then primed with a Not I -  
 oligo (dt) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pRT3  
 vector. Library is not normalized. Library was  
 constructed by Bento Soares and M. Fatima Bonaldo  
 (Soares)."

## ORIGIN

Query Match 55.5%; Score 548.6; DB 9; Length 620;  
 Best Local Similarity 95.7%; Pred. No. 2.5e-58;  
 Matches 596; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

QY 354 GCCACGCTTTGGCCCACTGGCGGCTCAATCCAGGCCAAGAGCGCTGGACCTGGGC 413  
 DB 620 GGCCAACTTTTGGCAAACTGGCGGCTCAATCCAGGCCAAGAGCGCTGGACCTGGGC 561

QY 414 ACCTTCAGGGGCTACTCCGCCCTGGCCCTGGCCCTGGCGCTGCGCGAGCGGCGCTG 473  
 DB 560 ACCTTCAGGGGCTACTCCGCCCTGGCCCTGGCCCTGGCGCGCTGCGCGAGCGGCGCTG 502  
 QY 474 GTGACCTCCAGAGCTGAGAGCGGAGCGCCCTGGAGCTGGAGCGGCCCTGTGAGAGCGCC 533  
 DB 501 GTGACCTCCAGAGCTGAGAGCGGAGCGCCCTGGAGCTGGAGCGGCCCTGTGAGAGCGCC 442  
 QY 534 GAGCGGAGCAACAAGATGACCTCCGGCTGAAGCCCGCTTGGAGACCTGGAGCGAGCTG 593  
 DB 441 GAGCGGAGCAACAAGATGACCTCCGGCTGAAGCCCGCTTGGAGACCTGGAGCGAGCTG 382  
 QY 594 CTGGCGGCGGCGAGCGCGGACCTTCGACGCTGGCGCTGGTGAATGCGAGCAAGAGAAC 653  
 DB 381 CTGGCGGCGGCGAGCGCGGACCTTCGACGCTGGCGCTGGTGAATGCGAGCAAGAGAAC 322  
 QY 654 TGCTCCGCTCTACGAGCGGCTGGCTGAGCTGCTGCGACCCCGAGGAGATCCTGGCGCTC 713  
 DB 321 T-CTCCGCTCTACGAGCGGCTGGCTGAGCTGCTGCGACCCCGAGGAGATCCTGGCGCTC 263  
 QY 714 CTCAGAGCTCTGTGGCGCGGAGAGTGTGCACTCCGAAAGGAGAGCTGGCGGCGAG 773  
 DB 262 CTCAGAGCTCTGTGGCGCGGAGAGTGTGCACTCCGAAAGGAGAGCTGGCGGCGAG 203  
 QY 774 TGTGTGCAAACTTAACGAAAGCATCGAGCGGAGCTGACGCTTCAATGACCTCTCTG 833  
 DB 202 TGTGTGCAAACTTAACGAAAGCATCGAGCGGAGCTGACGCTTCAATGACCTCTCTG 144  
 QY 834 CCCCTGGCGGAGTGAACCTTACCTTGGCTTCAAGATGAGAGGCTGGCCCTGTGAGTGG 893  
 DB 143 CCCCTGGCGGAGTGAACCTTACCTTGGCTTCAAGATGAGAGGCTGGCCCTGTGAGTGG 84  
 QY 894 CTCGAGGAGAGGTTGCTGGGAGCCCGAGGATGACCTTGAATTTAAATTCGAAATA 953  
 DB 83 CTCGAGGAGAGGTTGCTGGGAGCCCGAGGATGACCTTGAATTTAAATTCGAAATA 24  
 QY 954 AAGTGGGCGCTGGGACACGAAATA 976  
 DB 23 AAGTGGGCGCTGGGACACGAAATA 1

RESULT 31  
 CB194405 909 bp mRNA linear EST 05-FEB-2003  
 LOCUS AGENCOURT 11258413 NIH MGC 135 Mus musculus CDNA clone  
 DEFINITION IMAGE:30135806 5', mRNA sequence.  
 ACCESSION CB194405  
 VERSION CB194405.1 GI:28219021  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 1 (bases 1 to 909)  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. David Rowe

CDNA Library Preparation: Invitrogen Corp  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDAM0034 row: g column: 15  
 High quality sequence stop: 641.  
 Location/Qualifiers

## FEATURES

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 Normalized full-length enriched library from pooled mouse  
 embryonic limb, maxilla and mandible, day 12.5, 13.5,  
 14.5 and 15.5 (size selected for the 0.5-1 kb fragments)  
 cloned directionally, priming method: Oligo-dT. cDNA  
 enrichment: >1k bp. Average insert size 1.6k bp.  
 Normalization (Cot value): 7.5 kb. Priming sequence:  
 5'-GACTAGTCTAGATCGGAGCGGCCGCTT-3' Tissue contributed  
 by: David Rowe. Library constructed by ResGen, Invitrogen  
 Corp."

## ORIGIN

Query Match 54.9%; Score 542.8; DB 14; Length 909;  
 Best Local Similarity 82.6%; Pred. No. 1.1e-57;  
 Matches 634; Conservative 0; Mismatches 132; Indels 2; Gaps 1;

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63  CCGCCGCTCTCTGCGCCGCGCCATGACCCGCGTCTCGTGGCCGCGCG 122
    |||
3  CCGCGCTGCTAAGCTGACCAATGCTGACCGCTCCGCTATCTATCCAGCCGA 62
123 CTGGCCCTGAGCTCAAGGCACTGGGCGCGGCTTCCGCACTGGCTCTTCTGGGAGG 182
    |||
63 CTGGCCCTGAGCTCAAGGCACTGGGCGCGGCTTCCGCTATCTATCCAGCCGA 122
183 CCGTGGCCGCGCACTGGGCGCGGCAAGGCAAGTCTGCTTCCCGCGAGGACAGCCGC 242
123 CCGTGGCCCTCAATGGGCGGCTCCAGGCGGCAAGGCGCTGCTCCAGCTGAGACATATCC 182
243 CTGTGGCAATCTTCTGAGCGCTCCATGCGGAGGACACCCGCGCTCGAAGCTGAGG 302
183 CTGTGGCAATCTTCTGAGCGCTCCATGCGGAGGACACCCGCGCTCGAAGCTGAGG 242
303 CTGTGGCAATCTTCTGAGCGCTCCATGCGGAGGACACCCGCGCTCGAAGCTGAGG 242
243 CTGTGGCAATCTTCTGAGCGCTCCATGCGGAGGACACCCGCGCTCGAAGCTGAGG 302
363 TTGGCCCACTGGGCGCGGCTGATCAGGCGCAAGAGGCGCTGGAACCTTGCAG 422
303 CTGGCCCACTGGGCGCGGCTGATCAGGCGCAAGAGGCGCTGGAACCTTGCAG 362
423 GGGTACTTCCGCTGCGCTTGGCGCTGCGCTGCGCGGACCGGCGCGTGTGACCTGC 482
363 GGGTACTTCCGCTGCGCTTGGCGCTGCGCTGCGCGGACCGGCGCGTGTGACCTGC 422
483 GAGGTGACGCGGCGCGGCGGAGCTGGGAGCGGCGCTGTTGGAGGAGGCGGAGCGGAG 542
423 GAGGTGACGCGGCGCGGCGGAGCTGGGAGCGGCGCTGTTGGAGGAGGCGGAGCGGAG 482
543 CACAAGATGACCTCCGCGCTGAGACCGGCTTGGAGACCTTGGAGACCTTGGAGCGG 602
483 CACAAGATGACCTCCGCGCTGAGACCGGCTTGGAGACCTTGGAGACCTTGGAGCGG 542
603 GGGCAGGCGCGGACCTTGGAGCGGCGGCTTGGAGACCTTGGAGACCTTGGAGCGG 662
543 GGGCAGGCGCGGACCTTGGAGCGGCGGCTTGGAGACCTTGGAGACCTTGGAGCGG 602
663 TACTACGAGGCGCTCTGAGCGCTGAGACCGGAGGAGGAGGAGGAGGAGGAGGAGG 722
603 TACTACGAGGCGCTCTGAGCGCTGAGACCGGAGGAGGAGGAGGAGGAGGAGGAGG 662
723 CTGTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
663 CTGTGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
783 AACCTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 828
723 AACCTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 770
  
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RESULT 32

AI765658/c  
 LOCUS 572 bp mRNA linear EST 21-DEC-1998  
 DEFINITION w182g12.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2399878 3' similar to TR:085769 085769 HYPOTHETICAL 24.8 KD PROTEIN. // mRNA sequence.  
 ACCESSION AI765658 GI:5232167  
 VERSION AI765658  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE Homo sapiens  
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.  
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 COMMENT Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/bdnp/image/image.html  
 Insert Length: 974 Std Error: 0.00  
 Seq primer: -400p from Glpco  
 High quality sequence stop: 467.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2399878"  
 /tissue\_type="2 pooled tumors (clear cell type)"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Kid12"  
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 54.8%; Score 542; DB 9; Length 572;  
 Best Local Similarity 97.7%; Pred. No. 1.6e-57;  
 Matches 559; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

```

408 CTGGGCACTTTCACGCGGCTTCTGCGCTGCGCTGCGCTGCGCTGCGCGGAG 467
    |||
572 CTGGGCACTTTCACGCGGCTTCTGCGCTGCGCTGCGCTGCGCTGCGCGGAG 513
    |||
468 CGGTGTGACCTTTCACGCGGCTTCTGCGCTGCGCTGCGCTGCGCGGAG 527
    |||
512 CGGTGTGACCTTTCACGCGGCTTCTGCGCTGCGCTGCGCTGCGCGGAG 453
    |||
528 CAGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 587
    |||
452 CAGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 393
    |||
588 GAGCTGCTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 647
    |||
392 GAGCTGCTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 333
    |||
648 GAGACTGCTTCCGCTTCTACGAGGCGCTGCTGAGCTGCTGAGACCGGAGGAGCTTC 707
    |||
  
```

Db 332 GAGAACTGCTCCGCTACTACAGACGCGCTCTGACGCTGCTGCAACCCGAGGACATCTTC 273  
 QY 708 GCCGCTCTCAGAGT-CCTGTGGGCGGGAAGGTGCTGAACCTCCGAAAGGGGACGTGGC 766  
 Db 272 GCCGCTCTCAGAGTCCCTGTGGGCGGGAAGGTGCTGCAACCTCCGAAAGGGGACGTGGC 213  
 QY 767 GCGCGAGTGTGTGCGAAACCTTAACGACGATCCGGCGGAGCGTCAAGGCTTACATCAG 826  
 Db 212 GCGCGAGTGTGTGCGAAACCTTAACGACGATCCGGCGGAGCGTCAAGGCTTACATCAG 153  
 QY 827 CCGCCGCGCGCGGAGTGAAGTCACTTGGCTTCAAGATCTAGAGCTGGCCCTTACT 886  
 Db 152 CCGCTGCGCGCGGAGTGAAGTCACTTGGCTTCAAGATCTAGAGCTGGCCCTTACT 93  
 QY 887 GAGTGGGCTCGAGGAGGAGTGGCTGCGGAACCCGAGATTAAGCTGAGTTTAAATTC 946  
 Db 92 GAGTGGGCTCGAGGAGGAGTGGCTGCGGAACCCGAGATTAAGCTGAGTTTAAATTC 33  
 QY 947 GAAATTAAGTGGGCTGCGGAACCAAAAAA 978  
 Db 32 GAAATTAAGTGGGCTGCGGAACCAAAAAA 1

RESULT 33  
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 LOCUS 602812540F1 NCI CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4944633  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BG910899  
 VERSION BG910899.1 GI:14291375  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS NIH-MGC  
 TITLE NIH-MGC http://mgc.nci.nih.gov/.  
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
 COMMENT Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bhs-rc@mail.nih.gov  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILN at:  
 http://image.llnl.gov  
 Plate: ILN010889 row: p column: 10  
 High quality sequence stop: 614.

FEATURES  
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 1..639  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4944633"  
 /issue\_type="anaplastic oligodendroglioma with 1p/19q  
 loss"  
 /lab\_host="DH10B (71 phage-resistant)"  
 /clone\_lib="NCI CGAP\_Brn67"  
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site\_1: NCI;  
 Site\_2: Sall; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 2.3 kb. Constructed by Life  
 Technologies. Note: this is a NCI CGAP library."

## ORIGIN

Query Match 54.6%; Score 540.2; DB 12; Length 639;  
 Best Local Similarity 97.0%; Pred. No. 2.6e-57;  
 Matches 614; Conservative 0; Mismatches 13; Indels 6; Gaps 6;  
 QY 354 GCCACGCTTGGCCAGACGCGGCGGCTCATCAGCCAGAGAGCGCTGGACCTGGGC 413  
 Db 9 GCGCAGCTTGGCCAGACGCGGCGGCTCATCAGCCAGAGAGCGCTGGACCTGGGC 68

QY 414 ACCTTCAGGAGCTACTCCGCCCTGGCCCTTGAGCCCTGGC-GCTGCCCGGAGACGGGCGGT 472  
 Db 69 ACCTTCAGGAGCTACTCCGCCCTGGCCCTTGAGCCCTGGC-GCTGCCCGGAGACGGGCGGT 128  
 QY 473 GGTGACCTGAGAGTGAAGCGCGACGCCCGGAGTGGAGCGGCCCTGTGGAGCGAGC 532  
 Db 129 GGTGACCTGAGAGTGAAGCGCGACGCCCGGAGTGGAGCGGCCCTGTGGAGCGAGC 188  
 QY 533 CGAGGCGGAGCAAAAGATCGACCTCCGCTGAAGCCCGCTTGGAGACCTCGAGAGACT 592  
 Db 189 CGAGGCGGAGCAAAAGATCGACCTCCGCTGAAGCCCGCTTGGAGACCTCGAGAGACT 248  
 QY 593 GCTGCGGCGGAGCGAGCGCGGACCTTGGAGAGTGGCGTGGAGCGAGAGAGAG 652  
 Db 249 GCTGCGGCGGAGCGAGCGCGGACCTTGGAGAGTGGCGTGGAGCGAGAGAGAG 308  
 QY 653 CTGCTCGGCTTACTAGAGCGCTGCTGAGCTGCTGAGACCC-GAAGGCACTCTGCGCG 711  
 Db 309 CTGCTCGGCTTACTAGAGCGCTGCTGAGCTGCTGAGACCCGAGAGGCACTCTGCGCG 368  
 QY 712 TCCCTAGAGTCTGTGGCGCGGAGAGTGTGCGAACCTCCGAAAGGGACGTTGGGCGG 771  
 Db 369 TCCCTAGAGTCTGTGGCGCGGAGAGTGTGCGAACCTCCGAAAGGGACGTTGGGCGG 428  
 QY 772 AGTGTGTGCGAAACCTTAACGACGATCCGCGGAGAC-GTCAAGGCTTACATCAGCCTC 830  
 Db 429 AGTGTGTGCGAAACCTTAACGACGATCCGCGGAGAGTGTGCGAACCTTACATCAGCCTC 488  
 QY 831 CTGCCCTTGGGCGATGACCTACCTTGGGCTTCAAGATCTAGAGCTGGCCCTTACTAGT 890  
 Db 489 CTG-CCTGCGGCGAGTGAAGTCACTGCTGCTTCAAGATCTAGAGCTGG-CCTTACTAGT 546  
 QY 891 GGGCTCGAGGAGAGGTTGCTGCGGAG-CCCGAGAGTGAACCTGAGTTTAAATTCGAA 949  
 Db 547 GGGCTCGAGGAGAGGTTGCTGCGGAG-CCCGAGAGTGAACCTGAGTTTAAATTCGAA 606  
 QY 950 AATTAAGTGGGCTGCGGACACAAAAA 982  
 Db 607 AATTAAGTGGGCTGCGGACACAAAAA 639

RESULT 34  
 AW163525 566 bp mRNA linear EST 09-NOV-1999  
 LOCUS AW163525  
 DEFINITION au55h04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone  
 IMAGE:2784055 5' similar to TR:085769 085769 HYPOTHETICAL 24.8 KD  
 PROTEIN. ;, mRNA sequence.  
 ACCESSION AW163525  
 VERSION AW163525.1 GI:6302558  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (baes 1 to 566)  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
 Martin, J., Moore, B., Scheinberg, K., Stepoe, M., Tan, F.,  
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-NCI Human EST Project  
 Unpublished (1997)  
 Other ESTs: au55h04.x1  
 Contact: Wilson RK  
 Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

TITLE  
 JOURNAL  
 COMMENT  
 This clone is available royalty-free through ILN; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 377.



